

Ccl2 Cas9-CKO Strategy

Designer:

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Design Date:

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Project Overview

Project Name

Ccl2

Project type

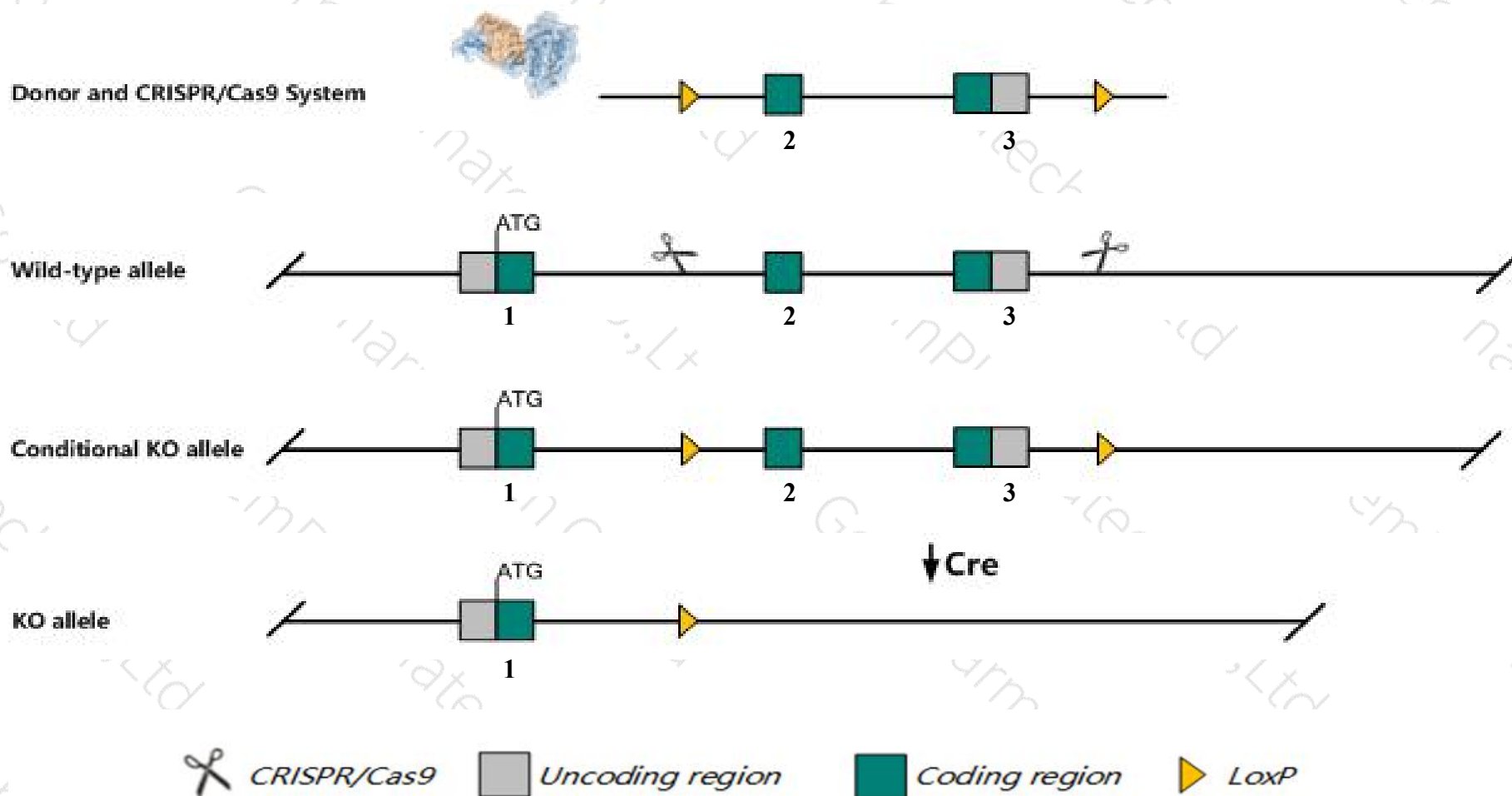
Cas9-CKO

Strain background

C57BL/6JGpt

Conditional Knockout strategy

This model will use CRISPR/Cas9 technology to edit the *Ccl2* gene. The schematic diagram is as follows:



Technical routes

- The *Ccl2* gene has 2 transcripts. According to the structure of *Ccl2* gene, exon2-exon3 of *Ccl2-201* (ENSMUST00000000193.5) transcript is recommended as the knockout region. The region contains 371bp coding sequence. Knock out the region will result in disruption of protein function.
- In this project we use CRISPR/Cas9 technology to modify *Ccl2* gene. The brief process is as follows: CRISPR/Cas9 system and Donor were microinjected into the fertilized eggs of C57BL/6JGpt mice. Fertilized eggs were transplanted to obtain positive F0 mice which were confirmed by PCR and sequencing. A stable F1 generation mouse model was obtained by mating positive F0 generation mice with C57BL/6JGpt mice.
- The flox mice will be knocked out after mating with mice expressing Cre recombinase, resulting in the loss of function of the target gene in specific tissues and cell types.

- According to the existing MGI data, Mice homozygous for a knock-out allele exhibit defective macrophage recruitment, abnormal choroid morphology, photoreceptor degeneration, and altered response to injury, infection, alcohol, and a high fat diet.
- The *Ccl2* gene is located on the Chr11. If the knockout mice are crossed with other mice strains to obtain double gene positive homozygous mouse offspring, please avoid the two genes on the same chromosome.
- This Strategy is designed based on genetic information in existing databases. Due to the complexity of biological processes, all risk of loxp insertion on gene transcription, RNA splicing and protein translation cannot be predicted at existing technological level.

Gene information (NCBI)

Ccl2 chemokine (C-C motif) ligand 2 [Mus musculus (house mouse)]

Gene ID: 20296, updated on 9-Apr-2019

Summary



Official Symbol Ccl2 provided by [MGI](#)

Official Full Name chemokine (C-C motif) ligand 2 provided by [MGI](#)

Primary source [MGI:MGI:98259](#)

See related [Ensembl:ENSMUSG00000035385](#)

Gene type protein coding

RefSeq status REVIEWED

Organism [Mus musculus](#)

Lineage Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Myomorpha; Muroidea; Muridae; Murinae; Mus; Mus

Also known as AI323594, HC11, JE, MCAF, MCP-1, MCP1, SMC-CF, Scya2, Sigje

Summary This gene is one of several cytokine genes clustered on chromosome 11. Chemokines are a superfamily of secreted proteins involved in immunoregulatory and inflammatory processes. The superfamily is divided into four subfamilies based on the arrangement of N-terminal cysteine residues of the mature peptide. This chemokine is a member of the CC subfamily which is characterized by two adjacent cysteine residues. This cytokine displays chemotactic activity for monocytes and memory T cells but not for neutrophils. The human ortholog has been implicated in the pathogenesis of diseases characterized by monocytic infiltrates, such as psoriasis, rheumatoid arthritis, and atherosclerosis. [provided by RefSeq, Sep 2015]

Expression Broad expression in genital fat pad adult (RPKM 4.2), stomach adult (RPKM 2.5) and 23 other tissues [See more](#)

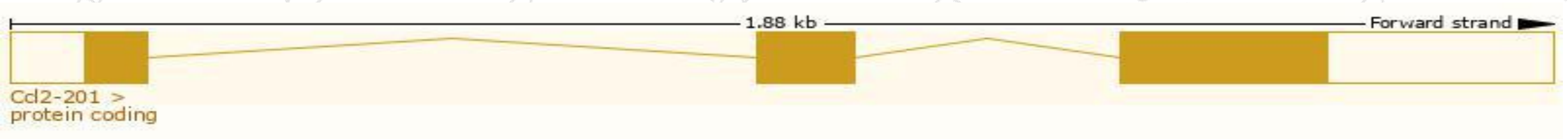
Orthologs [human](#) [all](#)

Transcript information (Ensembl)

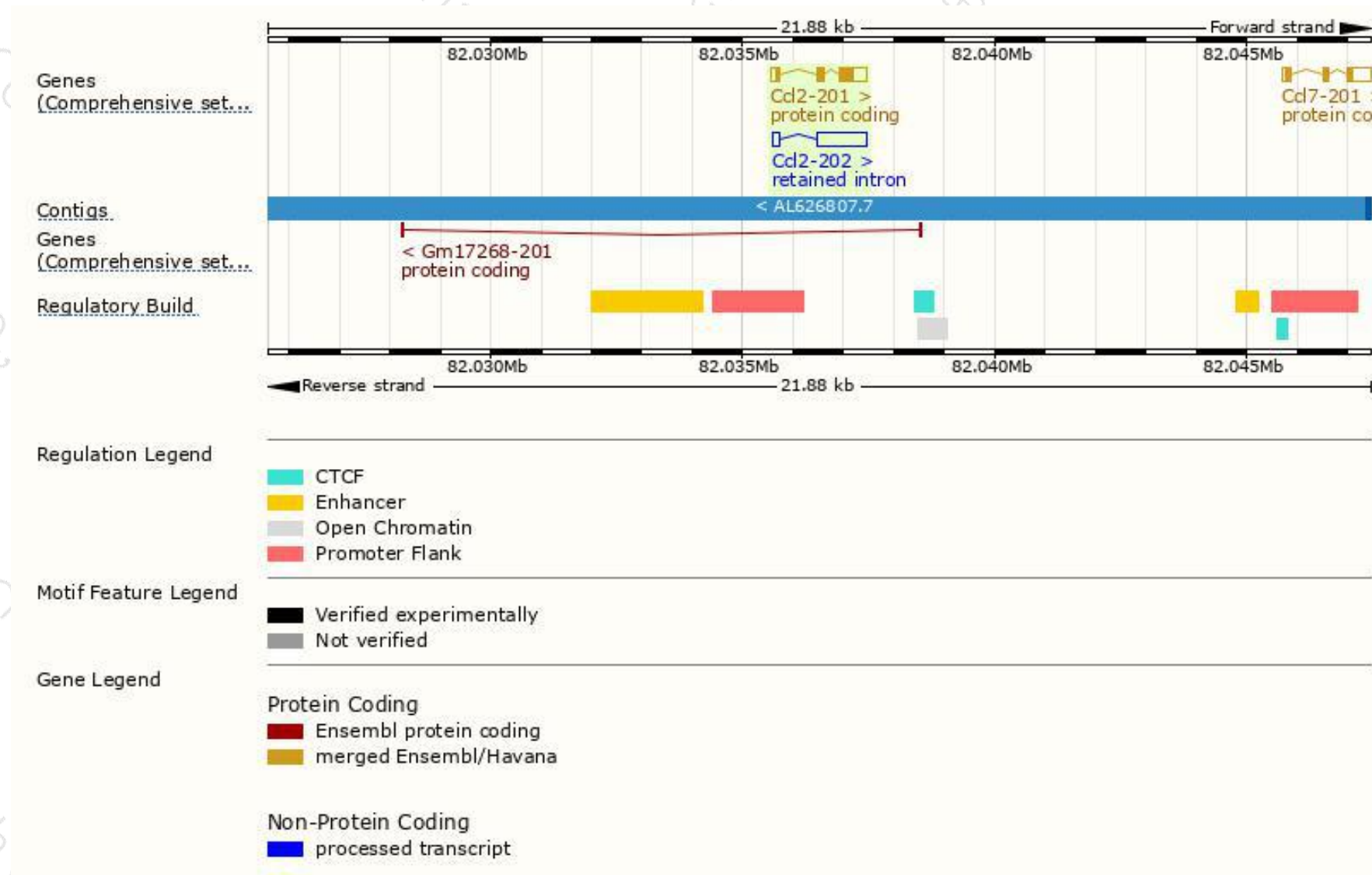
The gene has 2 transcripts,all transcripts are shown below:

Name	Transcript ID	bp	Protein	Biotype	CCDS	UniProt	Flags
Ccl2-201	ENSMUST00000000193.5	813	148aa	Protein coding	CCDS25139	P10148 Q5SVU3	TSL:1 GENCODE basic APPRIS P1
Ccl2-202	ENSMUST00000124479.1	1096	No protein	Retained intron	-	-	TSL:1

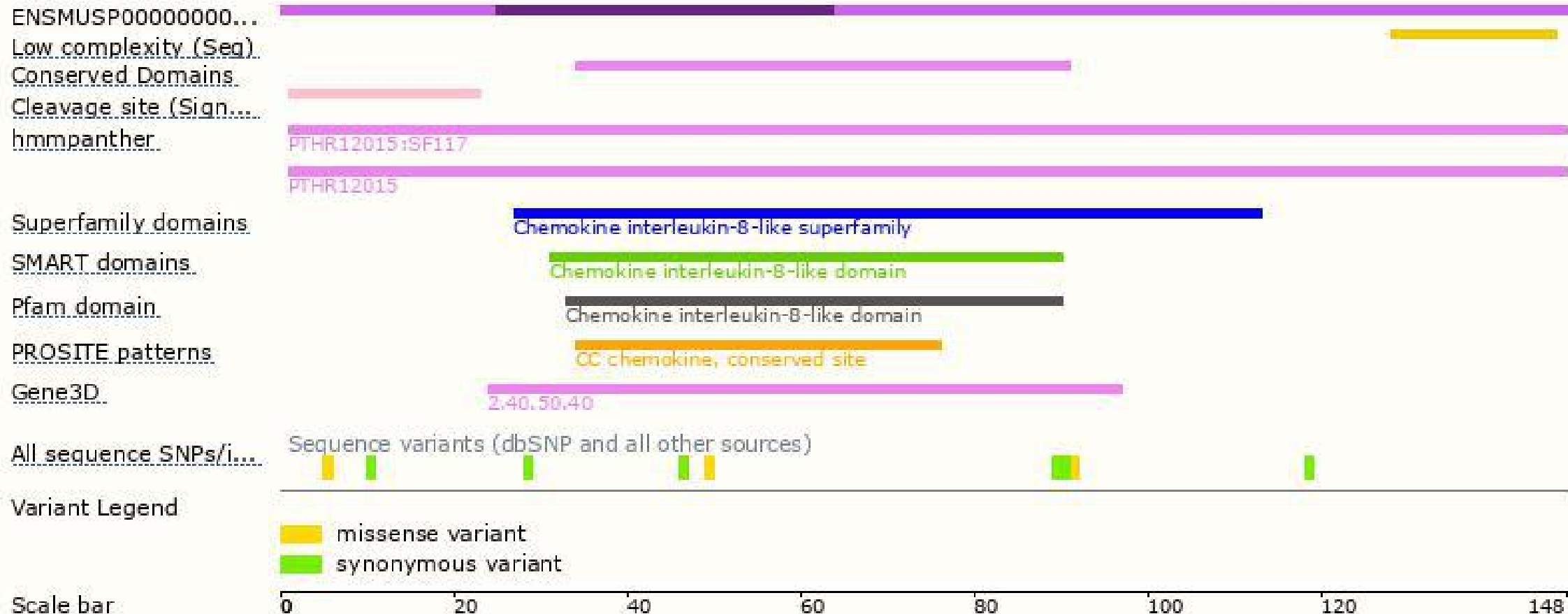
The strategy is based on the design of *Ccl2-201* transcript,The transcription is shown below



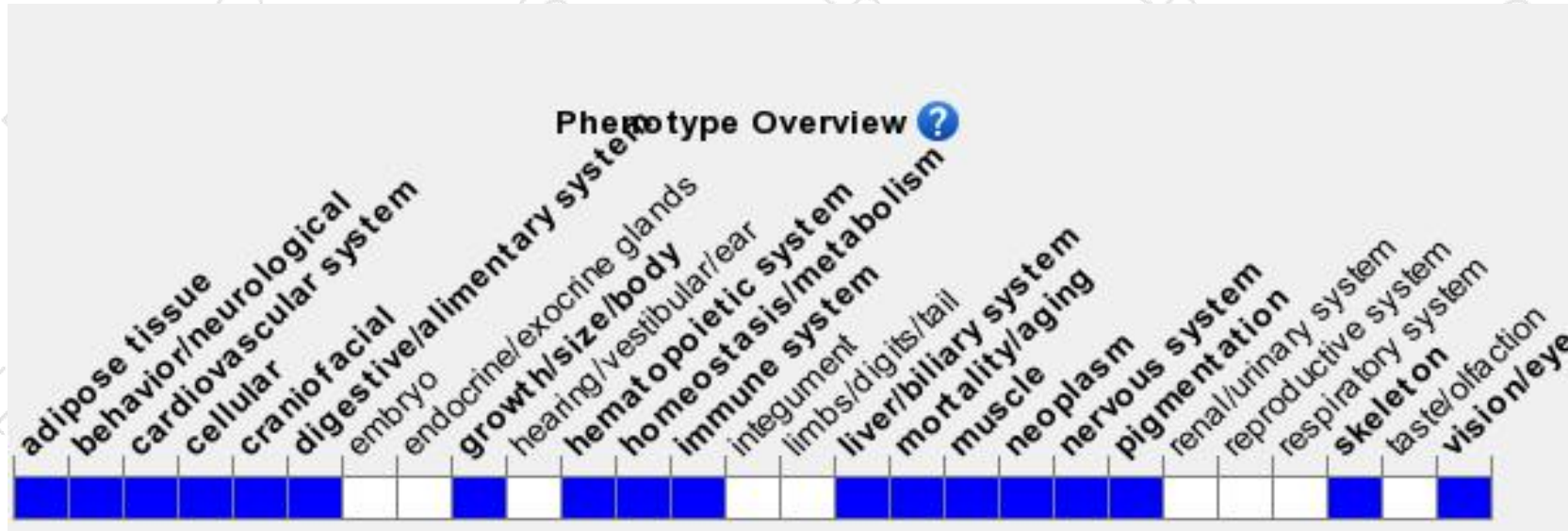
Genomic location distribution



Protein domain



Mouse phenotype description(MGI)



Phenotypes affected by the gene are marked in blue. Data quoted from MGI database(<http://www.informatics.jax.org/>).

According to the existing MGI data, Mice homozygous for a knock-out allele exhibit defective macrophage recruitment, abnormal choroid morphology, photoreceptor degeneration, and altered response to injury, infection, alcohol, and a high fat diet.

If you have any questions, you are welcome to inquire.

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